

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 4, 2005, 12:03:24 ; Search time 189 Seconds  
(without alignments)  
809.787 Million cell updates/sec

Title: US-10-006-867-2  
Perfect score: 1392  
Sequence: 1 MWFFQQLSFLPSALVIWTS.....YDTAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1825181 seqs, 575374646 residues  
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : 'UniProt 02:.'  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1392	100.0	266	2 Q6UX65	Q6ux65 homo sapien
2	1392	100.0	266	2 AAQ8856	Aaq8856 homo sapi
3	1245	89.4	267	2 Q9CR48	Q9cr48 m mus muscu
4	1235	88.7	267	2 Q9D520	Q9d520 mus musculu
5	1078	77.4	208	2 Q86VD3	Q86vd3 homo sapien
6	805.5	57.9	180	2 Q9D835	Q9d835 mus musculu
7	764.5	54.9	272	2 Q6IQ10	Q6iq10 brachydanio
8	764.5	54.9	272	2 AAH71426	Aah71426 brachydan
9	725	52.1	136	2 Q8NBQ4	Q8nbq4 homo sapien
10	492.5	35.4	238	2 Q8N682	Q8n682 homo sapien
11	479.5	34.4	238	2 Q9DC58	Q9dc58 mus musculu
12	479.5	34.4	238	2 BAB23366	Bab23366 mus muscu
13	471.5	33.9	287	2 Q6NRS6	Q6nrs6 xenopus lae
14	471.5	33.9	287	2 AAH70646	Aah70646 xenopus l
15	439.5	31.6	238	2 Q8QG82	Q8qgb2 oncorhynchu
16	388.5	27.9	282	2 Q7QE61	Q7qe61 anopheles g
17	361.5	26.0	246	2 O77262	O77262 drosophila
18	318.5	22.9	252	2 Q86F93	Q86f93 schistosoma
19	288	20.7	271	2 Q93319	Q93319 caenorhabdi
20	262	18.8	238	2 Q8R218	Q8r218 mus musculu
21	251.5	18.1	181	2 Q6XHF5	Q6xhf5 drosophila
22	251.5	18.1	181	2 AARI0251	Aar10251 drosophil
23	251	18.0	132	2 Q9NUN1	Q9nun1 homo sapien
24	251	18.0	132	2 AAH13773	Aah13773 homo sapi
25	240	17.2	132	2 Q78J26	Q78j26 mus musculu
26	203	14.6	249	2 Q8C8S3	Q8c8s3 mus musculu
27	201.5	14.5	271	2 Q6GFL4	Q6gpl4 xenopus lae
28	191.5	13.8	257	2 Q6IQJ3	Q6iqj3 brachydanio
29	191.5	13.8	257	2 AAH71413	Aah71413 brachydan
30	185.5	13.3	219	2 Q6P6P1	Q6p6p1 mus musculu
31	185.5	13.3	219	2 AAH62109	Aah62109 mus muscu

32	183.5	13.2	294	2 Q7SXX4	Q7sxx4 brachydanio
33	172.5	12.4	243	2 Q86IK0	Q86ik0 dictyosteli
34	161.5	11.6	123	2 Q8C9L9	Q8c9l9 mus musculu
35	160.5	11.5	271	2 Q86TG1	Q86tg1 homo sapien
36	157.5	11.3	271	2 Q9QZE9	Q9qze9 rattus norv
37	157.5	11.3	271	2 AAH72517	Aah72517 rattus no
38	151.5	10.9	271	2 Q91WN2	Q91wn2 mus musculu
39	150.5	10.8	243	2 Q86K17	Q86kl7 dictyosteli
40	120	8.6	224	2 Q23135	Q23135 caenorhabdi
41	112.5	8.1	252	2 Q9U3J7	Q9u3j7 caenorhabdi
42	112.5	8.1	252	2 CAB62801	Cab62801 caenorhab
43	106.5	7.7	140	2 Q8K117	Q8kl17 mus musculu
44	103	7.4	299	2 Q6CDS5	Q6cds5 yarrowia li
45	103	7.4	332	1 HMEC_ARCFU	O29749 archaeoglob

ALIGNMENTS

RESULT 1

Q6UX65					
ID	Q6UX65	PRELIMINARY;	PRT;	266	AA.
AC	Q6UX65;				
DT	05-JUL-2004	(TREMBlrel. 27, Created)			
DT	05-JUL-2004	(TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004	(TREMBlrel. 27, Last annotation update)			
DE	WWFQ154.				
GN	ORFNames=UNQ154;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22887296; PubMed=12975309;				
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,				
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,				
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,				
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,				
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,				
RA	Godowski P.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment."				
RL	Genome Res. 13:2265-2270(2003).				
DR	EMBL; AY358492; AAQ88856.1; -.				
SQ	SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;				

Query Match	100.0%;	Score 1392;	DB 2;	Length 266;
Best Local Similarity	100.0%;	Pred. No. 5.7e-108;		
Matches 266;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MWFFQQLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML	60	
Db	1	MWFFQQLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML	60	
Qy	61	NIAAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA	120	
Db	61	NIAAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA	120	
Qy	121	HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSSVL	180	
Db	121	HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSSVL	180	
Qy	181	HSGNFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRVEAN	240	
Db	181	HSGNFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRVEAN	240	
Qy	241	LHGLTLYDTAPCPINNERTRLLSRDI	266	

Db	241	LHGLTLYDTAPCPINNERTRLRSRD	266	
RESULT 2				
AAQ88856				
ID	AAQ88856	PRELIMINARY;	PRT;	266 AA.
AC	AAQ88856;			
DT	02-MAR-2004	(TrEMBLrel. 27, Created)		
DT	02-MAR-2004	(TrEMBLrel. 27, Last sequence update)		
DE	WWFQ154.			
GN	UNQ154.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=12975309;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The Secreted Protein Discovery Initiative (SPDI), a Large-Scale			
RT	Effort to Identify Novel Human Secreted and Transmembrane Proteins: A			
RT	Bioinformatics Assessment."			
RL	Genome Res. 13:2265-2270(2003).			
DR	EMBL; AY358492; AAQ88856.1; -.			
SQ	SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;			
Query Match 100.0%; Score 1392; DB 2; Length 266;				
Best Local Similarity 100.0%; Pred. No. 5.7e-108;				
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML	60	
Db	1	MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML	60	
QY	61	NIAAVLCIATIIYVRKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTTLFAA	120	
Db	61	NIAAVLCIATIIYVRKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTTLFAA	120	
QY	121	HVSGAVLTFGMSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCS	180	
Db	121	HVSGAVLTFGMSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCS	180	
QY	181	HSGNFGTDLQKHLWNPEDKGYVLHMITTAAEWSMSPSFFGFFLTYYIRDFQISLR	240	
Db	181	HSGNFGTDLQKHLWNPEDKGYVLHMITTAAEWSMSPSFFGFFLTYYIRDFQISLR	240	
QY	241	LHGLTLYDTAPCPINNERTRLRSRD	266	
Db	241	LHGLTLYDTAPCPINNERTRLRSRD	266	
RESULT 3				
Q9CR48				
ID	Q9CR48	PRELIMINARY;	PRT;	267 AA.
AC	Q9CR48;			
DT	01-JUN-2001	(TrEMBLrel. 17, Created)		
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)		
DT	01-OCT-2004	(TrEMBLrel. 28, Last annotation update)		
DE	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length			
DE	enriched library, clone:2610318G18 product:hypothetical protein, full			
DE	insert sequence (Mus musculus adult male tongue cDNA, RIKEN full-			
DE	length enriched library, clone:2310056E01 product:hypothetical			
DE	protein, full insert sequence) (Mus musculus 10 days lactation, adult			
DE	female mammary gland cDNA, RIKEN full-length enriched library,			

DE	clone:D730039I03 product:hypothetical protein, full insert			
DE	sequence).			
GN	Name=2610318G18Rik;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;			
RX	MEDLINE=99279253; PubMed=10349636;			
RA	Carninci P., Hayashizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Meth. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs.";			
RL	Nature 420:563-573(2002).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;			
RX	MEDLINE=20499374; PubMed=11042159;			
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,			
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;			
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to			
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";			
RL	Genome Res. 10:1617-1630(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;			
RX	MEDLINE=20530913; PubMed=11076861;			
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,			
RA	Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,			
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,			
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,			
RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,			
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,			
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;			
RT	"RIKEN integrated sequence analysis (RISA) system-384-format			
RT	sequencing pipeline with 384 multicapillary sequencer.";			
RL	Genome Res. 10:1757-1771(2000).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Tongue, and Whole body;			
RA	Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,			
RA	Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,			
RA	Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,			
RA	Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,			
RA	Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,			
RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,			
RA	Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,			
RA	Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,			
RA	Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,			
RA	Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,			
RA	Muramatsu M., Hayashizaki Y.;			
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Mammary gland;			
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,			
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,			
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,			



RESULT 5									
Q86VD3	Q86VD3								
ID	Q86VD3	PRELIMINARY;	PRT;	208 AA.					
AC	Q86VD3;								
DT	01-JUN-2003 (TReMBLrel. 24, Created)								
DT	01-MAR-2004 (TReMBLrel. 26, Last sequence update)								
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)								
DE	MGC54289 protein.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Eye;								
RX	MEDLINE=22388257; PubMed=12477932;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,								
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,								
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,								
RA	Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,								
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,								
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,								
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,								
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,								
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,								
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,								
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,								
RA	Jones S.J., Marra M.A.;								
RT	"Generation and initial analysis of more than 15,000 full-length human								
RT	and mouse cDNA sequences.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Eye;								
RA	Strausberg R.;								
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; BC047025; AAH47025.2; -.								
SQ	SEQUENCE 208 AA; 23352 MW; 35788E00AE9E4B35 CRC64;								
Query Match 77.4%; Score 1078; DB 2; Length 208;									
Best Local Similarity 100.0%; Pred. No. 6.7e-82;									
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	59	MLNIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLTF	118						
Db	1	MLNIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLTF	60						
QY	119	AAHVSAGVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVTCGVSALSLTCS	178						
Db	61	AAHVSAGVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVTCGVSALSLTCS	120						
QY	179	VLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYYIRDFQKISLRVE	238						
Db	121	VLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYYIRDFQKISLRVE	180						
QY	239	ANLHGLTLYDTAPCPINNERTRLLSRDI	266						
Db	181	ANLHGLTLYDTAPCPINNERTRLLSRDI	208						
RESULT 6									
Q9D835	Q9D835								
ID	Q9D835	PRELIMINARY;	PRT;	180 AA.					
AC	Q9D835;								
DT	01-JUN-2001 (TReMBLrel. 17, Created)								
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)								
DT	01-OCT-2004 (TReMBLrel. 28, Last annotation update)								
DE	Mus musculus adult male small intestine cDNA, RIKEN full-length								

DE enriched library, clone:2010305N14 product:hypothetical protein, full  
DE insert sequence (2610318G18Rik protein).  
GN Name=2010305N14Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Small intestine;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44 (1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Small intestine;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Small intestine;  
RX The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Small intestine;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Small intestine;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Small intestine;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,













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Db 168 PAVHDAGALITFCGVMYILQSYISKSCPTWNTTRATCHIRMTVSLIAFTAVVPMVSFVS 227
Qy 178 SVLHSGNFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYRDFQKISLRV 237
Db 228 --ILSG-----RKRLDWKPSDEGYPYHLTSAICENTWVAFGFMVYFLTFRDFQGVSIQI 279
Qy 238 EANLH 242
Db 280 STEIH 284

RESULT 14
AAH70646 PRELIMINARY; PRT; 287 AA.
AC AAH70646;
DT 13-MAY-2004 (TReMBLrel. 27, Created)
DT 13-MAY-2004 (TReMBLrel. 27, Last sequence update)
DT 13-MAY-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer M.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070646; AAH70646.1; -.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 287 AA; 31871 MW; 5E9814FA488BE462 CRC64;
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Matches 93; Conservative 56; Mismatches 79; Indels 17; Gaps 4;

Qy 3 WFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI 62

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Db 52 WCLQGAAPLPSILVWSSAGFLFSYIISVLIGHVPPFVPIYISDTGTSPPESGVFGFMISV 111
Qy 63 AAVLCIATYVRYKQVHALSPEENVIIK-----LNKAGLVGLSCLGLSIVANFQKTTL 117
Db 112 SAMLGAATMYTRY----MILERQNLSDIFLPIYFNKISLAIGLFGCIGMGIVATFQEMAV 167
Qy 118 FPAHVS GAVLTFGMGS LYM FVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCS 177
Db 168 PAVHDAGALITFCGVMYILQSYISKSCPTWNTTRATCHIRMTVSLIAFTAVVPMVSFVS 227
Qy 178 SVLHSGNFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYRDFQKISLRV 237
Db 228 --ILSG-----RKRLDWKPSDEGYPYHLTSAICENTWVAFGFMVYFLTFRDFQGVSIQI 279
Qy 238 EANLH 242
Db 280 STEIH 284

RESULT 15
Q8QGB2 PRELIMINARY; PRT; 238 AA.
AC Q8QGB2;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE VHSV-induced protein-6.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22129223; PubMed=12134009;
RA O'Farrell C., Vaghefi N., Cantonnet M., Buteau B., Boudinot P.,
RA Benmansour A.;
RT "Survey of transcript expression in rainbow trout leukocytes reveals a
RT major contribution of interferon-responsive genes in the early
RT response to a rhabdovirus infection.";
RL J. Virol. 76:8040-8049 (2002).
DR EMBL; AF483532; AAM18471.1; -.
SQ SEQUENCE 238 AA; 26650 MW; 06BEDE247670D134 CRC64;

Query Match 31.6%; Score 439.5; DB 2; Length 238;
Best Local Similarity 40.3%; Pred. No. 1.3e-28;
Matches 96; Conservative 45; Mismatches 88; Indels 9; Gaps 4;

Qy 1 MWWFQQLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MLWFMEGICFLPISLVIMSSSTFIVSYLIALFEDVDVIFPYISDTGAEPPESCVFGMLT 60
Qy 61 NIAAVLCIATYVRYKQVHALSPEE-NVIIKLNKAGLVGLSCLGLSIVANFQKTTLFA 119
Db 61 VITAFAGMATMYARYKFVEKLNKAGGVRRPSLNQAQAFWIGMLSCIGMCFVATFQETTITA 120
Qy 120 AHVSGAVLTFGMGS LYM FVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSV 179
Db 121 VHDAGAILFFVSGVLYTILQSIISYKAFP--YGCSLALCR---VRTGMATIAFLAVFPT 174
Qy 180 LHSGNFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYRDFQKISLRV 237
Db 175 VVCAIFVT--QTTLHRKTEDEDNVFHLVSAVSEWIVAFSIFLFFFTYIHLKKFTKL 230
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